

ATTACHED TO  
#10

SEQUENCE LISTING

<110> DORKEN, Bernd  
RIETHMULLER, Gert  
KUFER, Peter  
LUTTERBUSE, Ralf  
BARGOU, Ralf  
LOFFLER, Anja

<120> CD19XCD3 SPECIFIC POLYPEPTIDES AND USES THEREOF

<130> 028622/0102

<140> US 09/673,735

<141> 2000-12-27

<150> PCT/EP99/02693

<151> 1999-04-21

<150> EP 98107269.7

<151> 1998-04-21

<160> 13

<170> PatentIn version 3.1

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

gaagcagcg tagatattct gmtaccacaa wctcca

36

<210> 2

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

gaagatggat ccagcggccg cagcatcagc

30

<210> 3

<211> 33

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Primer  
  
 <400> 3  
 cagccggcca tggcgcaggt scagctgcag sag 33  
  
 <210> 4  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 4  
 accaggggcc agtggataga caagcttggg tgtcgtttt 39  
  
 <210> 5  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 5  
 aggtgtacac tccatatcca gctgaccag tctcca 36  
  
 <210> 6  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 6  
 ggagccgccc ccgccagaac caccaccttt gatctcgagc ttggtccc 48  
  
 <210> 7  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 7  
 ggcggcggcg gctccggtgg tgggtgttct caggtactgc agagtcgg 48

<210> 8  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 8  
 aatccggagg agacgggtgac cgtgggtccct tggccccag

39

<210> 9  
 <211> 1611  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (11)..(1603)  
 <223>

<400> 9  
 gaattccacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr  
 1 5 10

49

gct aca ggt gtc cac tcc gac tac aaa gat gat gac gat aag gat atc  
 Ala Thr Gly Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile  
 15 20 25

97

cag ctg acc cag tct cca gct tct ttg gct gtg tct cta ggg cag agg  
 Gln Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg  
 30 35 40 45

145

gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt gat  
 Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp  
 50 55 60

193

agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa ctc  
 Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu  
 65 70 75

241

ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg ttt  
 Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe  
 80 85 90

289

agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct gtg  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val  
 95 100 105

337

gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag gat  
 Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp  
 110 115 120 125

385

ccg tgg acg ttc ggt gga ggg acc aag ctc gag atc aaa ggt ggt ggt	433
Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly	
130 135 140	
ggt tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct cag gtg cag ctg	481
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu	
145 150 155	
cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag att	529
Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile	
160 165 170	
tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac tgg	577
Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp	
175 180 185	
gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att tgg	625
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp	
190 195 200 205	
cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa gcc	673
Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala	
210 215 220	
act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc agc	721
Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser	
225 230 235	
agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg gag	769
Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu	
240 245 250	
act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggc caa	817
Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln	
255 260 265	
ggg acc acg gtc acc gtc tcc tcc gga ggt ggt gga tcc gat atc aaa	865
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Lys	
270 275 280 285	
ctg cag cag tca ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag	913
Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	
290 295 300	
atg tcc tgc aag act tct ggc tac acc ttt act agg tac acg atg cac	961
Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His	
305 310 315	
tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att	1009
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile	
320 325 330	
aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag	1057
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys	
335 340 345	

gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg	1105
Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu	
350 355 360 365	
agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat	1153
Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr	
370 375 380	
tat gat gat cat tac tgc ctt gac tac tgg ggc caa ggc acc act ctc	1201
Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu	
385 390 395	
aca gtc tcc tca gtc gaa ggt gga agt gga ggt tct ggt gga agt gga	1249
Thr Val Ser Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly	
400 405 410	
ggt tca ggt gga gtc gac gac att cag ctg acc cag tct cca gca atc	1297
Gly Ser Gly Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile	
415 420 425	
atg tct gca tct cca ggg gag aag gtc acc atg acc tgc aga gcc agt	1345
Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	
430 435 440 445	
tca agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc	1393
Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser	
450 455 460	
ccc aaa aga tgg att tat gac aca tcc aaa gtg gct tct gga gtc cct	1441
Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro	
465 470 475	
tat cgc ttc agt ggc agt ggg tct ggg acc tca tac tct ctc aca atc	1489
Tyr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
480 485 490	
agc agc atg gag gct gaa gat gct gcc act tat tac tgc caa cag tgg	1537
Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
495 500 505	
agt agt aac ccg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa	1585
Ser Ser Asn Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys	
510 515 520 525	
cat cat cac cat cat cat tagtcgac	1611
His His His His His His	
530	

<210> 10  
 <211> 531  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Ile Gln Leu Thr  
20 25 30

Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile  
35 40 45

Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu  
50 55 60

Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
65 70 75 80

Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser  
85 90 95

Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val  
100 105 110

Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr  
115 120 125

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly  
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser  
145 150 155 160

Gly Ala Glu Leu Val Arg Pro Gly Ser Ser Val Lys Ile Ser Cys Lys  
165 170 175

Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn Trp Val Lys Gln  
180 185 190

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp  
195 200 205

Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr  
 210 215 220

Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala  
 225 230 235 240

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr  
 245 250 255

Val Gly Arg Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr  
 260 265 270

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln  
 275 280 285

Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys  
 290 295 300

Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys  
 305 310 315 320

Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser  
 325 330 335

Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu  
 340 345 350

Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu  
 355 360 365

Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp  
 370 375 380

His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser  
 385 390 395 400

Ser Val Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly  
 405 410 415

Gly Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala  
 420 425 430

Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val  
435 440 445

Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg  
450 455 460

Trp Ile Tyr Asp Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe  
465 470 475 480

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met  
485 490 495

Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn  
500 505 510

Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys His His His  
515 520 525

His His His  
530

<210> 11  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide Linker

<400> 11

Gly Gly Gly Gly Ser  
1 5

<210> 12  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 12

Asp Tyr Lys Asp  
1



<210> 13  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Polypeptide Linker

<400> 13

B5  
Wt  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

---